ABSTRACT

DIFFERENTIAL SCREENING

The invention concerns a method for identifying and/or cloning nucleic acid regions representing qualitative differences associated with alternative splicing events and/or with insertions, deletions located in RNA transcribed genome regions, between two physiological situations, comprising either hybridization of RNA derived from the test situation with cDNA's derived from the reference situation and/or reciprocally, or double-strand hybridization of cDNA derived from the test situation with cDNA's derived from the reference situation; and identifying and/or cloning nucleic acids representing qualitative differences. The invention also concerns compositions or banks of nucleic acids representing qualitative differences between two physiological situations, obtainable by the above method, and their use as probe, for identifying genes or molecules of interest, or still for example in methods of pharmacogenomics, and profiling of molecules relative to their therapeutic and/or toxic effects. The invention further concerns the use of dysregulation of splicing RNA as markers for predicting molecule toxicity and/or efficacy, and as markers in pharmacogenomics.